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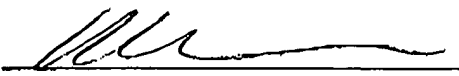
Pages 11 and 12 of the specification provide the correct sequences of the recited EST yu23d11 and yq76e12 below the corresponding H-Robo1 sequences. While the recited EST, the recited H-Robo1 sequences, SEQ ID NO:7 and SEQ ID NO:8 are all correct, the specification contains three minor errors correlating the sequence position number from the SEQ ID NOS with the recited sequences. In particular, careful examination of SEQ ID NO:8 shows that the H-Robo1 portions recited on pages 11 and 12 (which correspond to the two excluded EST translates) are residues 168-217 and 1316-1520, respectively. SEQ ID NO:7 codes for SEQ ID NO:8, so the corresponding portions of SEQ ID NO:7 are 502-651 and 3946-4560, respectively. Unfortunately, these corresponding portions of the SEQ ID NOS were not all correctly identified in the specification.

We enclose copies of pages 58, 60, 61 and 65 of the application, marked up to identify the H-Robo1 sequences recited on pages 11-12 and the corresponding coding sequences.

We apologize for the unnecessary confusion caused by the errors in our specification. We note that the amended claims were correct, that all the correct sequence data, SEQ ID NOS and provisos are properly contained in the application, that it was only three cross-references between the recited sequences and the SEQ ID NOS that were erroneous and that these amendments, correcting the cross-references, introduce no new matter.

Upon allowability of the product claims of elected Group II (claims 10-42 and 50-67), Applicants request joinder of method claims 43-49 (in the case of an elected product claim, rejoinder will be permitted when a product claim is found allowable and the withdrawn process claim depends from or otherwise includes all the limitations of an allowed product claim, per Commissioner Lehman's Notice of February 28, 1996: Guidance on Treatment of Product and Process Claims in light of *In re Ochiai*, *In re Brouwer* and 35 U.S.C. 103(b)).

Respectfully submitted,  
SCIENCE & TECHNOLOGY LAW GROUP

  
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encl. Pages 58, 60, 61 and 65.

1250 1255 1260  
 Ala Ser Thr Leu Ala His Ser Cys Tyr Gly Thr Asn Gly Thr Ala Gln  
 1265 1270 1275 1280  
 Arg Phe Arg Ser Ile Pro Arg Asn Asn Gly Ile Val Thr Gln Glu Gln  
 1285 1290 1295  
 Thr

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4956 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGAAATGGA AACATGTTCC TTTTTTGGTC ATGATATCAC TCCTCAGCTT ATCCCCAAAT	60
CACCTGTTTC TGGCCCAGCT TATTCCAGAC CCTGAAGATG TAGAGAGGGG GAACGACCAC	120
GGGACGCCAA TCCCCACCTC TGATAACGAT GACAATTCCG TGGGCTATAC AGGCTCCCGT	180
CTTCGTCAGG AAGATTTTCC ACCTCGCATT GTTGAACACC CTTCAGACCT GATTGTCTCA	240
AAAGGAGAAC CTGCAACTTT GAACTGCAAA GCTGAAGGCC GCCCCACACC CACTATTGAA	300
TGGTACAAAG GGGGAGAGAG AGTGGAGACA GACAAAGATG ACCCTCGCTC ACACCGAATG	360
TTGCTGCCGA GTGGATCTTT ATTTTCTTA CGTATAGTAC ATGGACGGAA AAGTAGACCT	420
GATGAAGGAG TCTATGTCTG TGTAGCAAGG AATTACCTTG GAGAGGCTGT GAGCCACAAT	480
GCATCGCTGG AAGTAGCCAT A <sup>50</sup> TTTCGGGAT GACTTCAGAC AAAACCCCTT GGATGTCATG	540
GTTGCAGTAG GAGAGCCTGC AGTAATGGAA TGCCAACCTC CACGAGGCCA TCCTGAGCCC	600
ACCATTTTCAT GGAAGAAAGA TGGCTCTCCA CTGGATGATA AAGATGAAAG <sup>550</sup> ATAACTATA	660
CGAGGAGGAA AGCTCATGAT CACTTACACC CGTAAAAGTG ACGCTGGCAA ATATGTTTGT	720
GTTGGTACCA ATATGGTTGG GGAACGTGAG AGTGAAGTAG CCGAGCTGAC TGTCTTAGAG	780
AGACCATCAT TTGTGAAGAG ACCCAGTAAC TTGGCAGTAA CTGTGGATGA CAGTGCAGAA	840
TTTAAATGTG AGGCCCGAGG TGACCCTGTA CCTACAGTAC GATGGAGGAA AGATGATGGA	900
GAGCTGCCCA AATCCAGATA TGAAATCCGA GATGATCATA CCTTGAAAAT TAGGAAGGTG	960
ACAGCTGGTG ACATGGGTTT ATACACTTGT GTTGCAGAAA ATATGGTGGG CAAAGCTGAA	1020
GCATCTGCTA CTCTGACTGT TCAAGAACCT CCACATTTTG TTGTGAAACC CCGTGACCAG	1080
GTTGTTGCTT TGGGACGGAC TGTAACCTTT CAGTGTGAAG CAACCGGAAA TCCTCAACCA	1140
GCTATTTTCT GGAGGAGAGA AGGGAGTCAG AATCTACTTT TCTCATATCA ACCACCACAG	1200
TCATCCAGCC GATTTTCAGT CTCCCAGACT GGCGACCTCA CAATTACTAA TGTCCAGCGA	1260
TCTGATGTTG GTTATTACAT CTGCCAGACT TTAAATGTTG CTGGAAGCAT CATCACAAAG	1320
GCATATTTGG AAGTTACAGA TGTGATTGCA GATCGGCCTC CCCCAGTTAT TCGACAAGGT	1380

GCAAGGATGT ATTTGCAACA AGATGAATTA GAAGAGGAGG AAGATGAACG AGGCCCCACT 3720  
 CCCCTGTTC GGGGAGCAGC TTCTTCTCCA GCTGCCGTGT CCTATAGCCA TCAGTCCACT 3780  
 GCCACTCTGA CTCCCTCCCC ACAGGAAGAA CTCCAGCCCA TGTTACAGGA TTGTCCAGAG 3840  
 GAGACTGGCC ACATGCAGCA CCAGCCCGAC AGGAGACGGC AGCCTGTGAG TCCTCCTCCA 3900  
 CCACCACGGC CGATCTCCCC TCCACATACC TATGGCTACA TTCA<sup>E</sup>GACC CCTGGTCTCA 3960  
 GATATGGATA CGGATGCGCC AGAAGAGGAA GAAGACGAAG CCGACATGGA GGTAGCCAAG 4020  
 ATGCAAACCA GAAGGCTTTT GTTACGTGGG CTTGAGCAGA CACCTGCCTC CAGTGTGGG 4080  
 GACCTGGAGA GCTCTGTCAC GGGGTCCATG ATCAACGGCT GGGGCTCAGC CTCAGAGGAG 4140  
 GACAACATTT CCAGCGGACG CTCCAGTGTT AGTTCTTCGG ACGGCTCCTT TTTCAGTGAT 4200 yq 76e.12  
 GCTGACTTTG CCCAGGCAGT CGCAGCAGCG GCAGAGTATG CTGGTCTGAA AGTAGCACGA 4260  
 CGGCAAATGC AGGATGCTGC TGGCCGTCGA CATTTTCATG CGTCTCAGTG CCCTAGGCCC 4320  
 ACAAGTCCCG TGTCTACAGA CAGCAACATG AGTGCCGCCG TAATGCAGAA AACCAGACCA 4380  
 GCCAAGAAAC TGAAACACCA GCCAGGACAT CTGCGCAGAG AAACCTACAC AGATGATCTT 4440  
 CCACCACCTC CTGTGCCGCC ACCTGCTATA AAGTCACCTA CTGCCCCAATC CAAGACACAG 4500  
 CTGGAAGTAC GACCTGTAGT GGTGCCAAAA CTCCCTTCTA TGGATGCAAG AACAGACAGA 4560  
 TCATCAGACA GAAAAGGAAG CAGTTACAAG GGGAGAGAAG TGTTGGATGG AAGACAGGTT 4620  
 GTTGACATGC GAACAAATCC AGGTGATCCC AGAGAAGCAC AGGAACAGCA AAATGACGGG 4680  
 AAAGGACGTG GAAACAAGGC AGCAAAACGA GACCTTCCAC CAGCAAAGAC TCATCTCATC 4740  
 CAAGAGGATA TTCTACCTTA TTGTAGACCT ACTTTTCCAA CATCAAATAA TCCCAGAGAT 4800  
 CCCAGTTTCT CAAGCTCAAT GTCATCAAGA GGATCAGGAA GCAGACAAAG AGAACAAGCA 4860  
 AATGTAGGTC GAAGAAATAT TGCAGAAATG CAGGTA<sup>E</sup>CTTG GAGGATATGA AAGAGGAGAA 4920  
 GATAATAATG AAGAATTAGA GGAAACTGAA AGCTGA 4956

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1651 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Lys Trp Lys His Val Pro Phe Leu Val Met Ile Ser Leu Leu Ser

1 5 10 15

Leu Ser Pro Asn His Leu Phe Leu Ala Gln Leu Ile Pro Asp Pro Glu

20 25 30

Asp Val Glu Arg Gly Asn Asp His Gly Thr Pro Ile Pro Thr Ser Asp

35 40 45

Asn Asp Asp Asn Ser Leu Gly Tyr Thr Gly Ser Arg Leu Arg Gln Glu

50 55 60  
Asp Phe Pro Pro Arg Ile Val Glu His Pro Ser Asp Leu Ile Val Ser  
65 70 75 80  
Lys Gly Glu Pro Ala Thr Leu Asn Cys Lys Ala Glu Gly Arg Pro Thr  
85 90 95  
Pro Thr Ile Glu Trp Tyr Lys Gly Gly Glu Arg Val Glu Thr Asp Lys  
100 105 110  
Asp Asp Pro Arg Ser His Arg Met Leu Leu Pro Ser Gly Ser Leu Phe  
115 120 125  
Phe Leu Arg Ile Val His Gly Arg Lys Ser Arg Pro Asp Glu Gly Val  
130 135 140  
Tyr Val Cys Val Ala Arg Asn Tyr Leu Gly Glu Ala Val Ser His Asn  
145 150 155 160  
Ala Ser Leu Glu Val Ala Ile [Leu Arg Asp Asp Phe Arg Gln Asn Pro  
165 170 175  
Ser Asp Val Met Val Ala Val Gly Glu Pro Ala Val Met Glu Cys Gln  
180 185 190  
Pro Pro Arg Gly His Pro Glu Pro Thr Ile Ser Trp Lys Lys Asp Gly  
195 200 205  
Ser Pro Leu Asp Asp Lys Asp Glu Arg ] Ile Thr Ile Arg Gly Gly Lys  
210 215 220  
Leu Met Ile Thr Tyr Thr Arg Lys Ser Asp Ala Gly Lys Tyr Val Cys  
225 230 235 240  
Val Gly Thr Asn Met Val Gly Glu Arg Glu Ser Glu Val Ala Glu Leu  
245 250 255  
Thr Val Leu Glu Arg Pro Ser Phe Val Lys Arg Pro Ser Asn Leu Ala  
260 265 270  
Val Thr Val Asp Asp Ser Ala Glu Phe Lys Cys Glu Ala Arg Gly Asp  
275 280 285  
Pro Val Pro Thr Val Arg Trp Arg Lys Asp Asp Gly Glu Leu Pro Lys  
290 295 300  
Ser Arg Tyr Glu Ile Arg Asp Asp His Thr Leu Lys Ile Arg Lys Val  
305 310 315 320  
Thr Ala Gly Asp Met Gly Ser Tyr Thr Cys Val Ala Glu Asn Met Val  
325 330 335  
Gly Lys Ala Glu Ala Ser Ala Thr Leu Thr Val Gln Glu Pro Pro His  
340 345 350  
Phe Val Val Lys Pro Arg Asp Gln Val Val Ala Leu Gly Arg Thr Val

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1265 1270 1275 1280  
Glu Thr Gly His Met Gln His Gln Pro Asp Arg Arg Arg Gln Pro Val  
1285 1290 1295  
Ser Pro Pro Pro Pro Pro Arg Pro Ile Ser Pro Pro His Thr Tyr Gly  
1300 1305 1310  
Tyr Ile Ser [Gly Pro Leu Val Ser Asp Met Asp Thr Asp Ala Pro Glu  
1315 1320 1325  
Glu Glu Glu Asp Glu Ala Asp Met Glu Val Ala Lys Met Gln Thr Arg  
1330 1335 1340  
Arg Leu Leu Leu Arg Gly Leu Glu Gln Thr Pro Ala Ser Ser Val Gly  
1345 1350 1355 1360  
Asp Leu Glu Ser Ser Val Thr Gly Ser Met Ile Asn Gly Trp Gly Ser  
1365 1370 1375  
Ala Ser Glu Glu Asp Asn Ile Ser Ser Gly Arg Ser Ser Val Ser Ser  
1380 1385 1390  
Ser Asp Gly Ser Phe Phe Thr Asp Ala Asp Phe Ala Gln Ala Val Ala  
1395 1400 1405  
Ala Ala Ala Glu Tyr Ala Gly Leu Lys Val Ala Arg Arg Gln Met Gln  
1410 1415 1420  
Asp Ala Ala Gly Arg Arg His Phe His Ala Ser Gln Cys Pro Arg Pro  
1425 1430 1435 1440  
Thr Ser Pro Val Ser Thr Asp Ser Asn Met Ser Ala Ala Val Met Gln  
1445 1450 1455  
Lys Thr Arg Pro Ala Lys Lys Leu Lys His Gln Pro Gly His Leu Arg  
1460 1465 1470  
Arg Glu Thr Tyr Thr Asp Asp Leu Pro Pro Pro Pro Val Pro Pro Pro  
1475 1480 1485  
Ala Ile Lys Ser Pro Thr Ala Gln Ser Lys Thr Gln Leu Glu Val Arg  
1490 1495 1500  
Pro Val Val Val Pro Lys Leu Pro Ser Met Asp Ala Arg Thr Asp Arg ]  
1505 1510 1515 1520  
Ser Ser Asp Arg Lys Gly Ser Ser Tyr Lys Gly Arg Glu Val Leu Asp  
1525 1530 1535  
Gly Arg Gln Val Val Asp Met Arg Thr Asn Pro Gly Asp Pro Arg Glu  
1540 1545 1550  
Ala Gln Glu Gln Gln Asn Asp Gly Lys Gly Arg Gly Asn Lys Ala Ala  
1555 1560 1565  
Lys Arg Asp Leu Pro Pro Ala Lys Thr His Leu Ile Gln Glu Asp Ile

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